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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:38:30; Search time 95 Seconds

(without alignments)

1178.804 Million cell updates/sec

February 21, 2006, 05:38:30; Search time 95 Seconds

(without alignments)

1178.804 Million cell updates/sec

Sequence: 1 gagetctctccgaggtggg......gctatattagagggagcgaa 63

Scoring table: DENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID Description Match Length DB ID Description Match Length DB ID Description Sequence 15, Appl 2 13.6 53.3 129 2 105.09-193-853-15 Sequence 15, Appl 3 13.6 53.3 129 2 105.09-193-853-15 Sequence 15, Appl 2 13.6 53.3 140 2 105.09-193-853-15 Sequence 15, Appl 2 13.6 53.3 150 2 105.09-193-853-19 Sequence 19, Appl 10 13.6 53.3 161 2 105.09-193-853-19 Sequence 19, Appl 11 13.6 53.3 161 2 105.09-193-853-19 Sequence 18, Appl 11 13.6 53.3 164 3 105.09-193-853-19 Sequence 18, Appl 11 13.6 53.3 164 3 105.09-193-853-19 Sequence 26, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 11 13.6 53.3 168 2 105.09-193-853-4 Sequence 27, Appl 12 13.6 53.3 168 3 105.09-193-853-4 Sequence 27, Appl 12 13.6 53.3 201 3 105.09-193-853-2 Sequence 27, Appl 12 13.6 53.3 201 3 105.09-193-853-4 Sequence 27, Appl 12 13.6 53.3 201 3 105.09-813-254A-1 Sequence 27, Appl 12 13 13.6 53.3 201 3 105.09-813-224A-1 Sequence 27, Appl 12 13 13.6 53.3 201 3 105.09-813-224A-1 Sequence 27, Appl 12 13 13.6 53.3 201 3 105.09-813-224A-1 Sequence 27, Appl 12 23 33.6 53.3 258 2 105.09-813-224A-1 Sequence 27, Appl 22 33.6 53.3 258 2 105.09-813-224-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 33.6 53.3 201 3 105.09-202-316-4 Sequence 24, Appl 22 300-202-316-4 Sequence 24, Appl 22 300-202

| Sequence 10, Appl sequence 10, Appl Sequence 10, Appl Sequence 21, Appl Sequence 28, Appl Sequence 27, Appl Sequence 27, Appl Sequence 3, Appl Sequence 3, Appl Sequence 1, Appl Sequence 19, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11, Ap | Length 127; Indels 0; Gaps | GGAGCGAA 63 GGAGCGAA 100 | |
|--|--|--|---|
| US-09-202-316-7 US-08-189-256A-10 US-08-193-853-10 US-09-193-853-10 US-09-193-853-28 US-09-193-853-28 US-09-193-853-28 US-09-193-853-28 US-09-193-853-3 US-09-217-360-15 US-09-217-360-16 US-09-217-360-16 US-09-217-360-16 US-09-217-360-16 US-09-283-419-1 ALIGNMENTS ALIGNMENTS PROCESSES FOR PREPARATION US/09/635,132 US-09-283-132 US-09-283-132 US-09-283-132 | . Score 33.6; DB 3; Pred. No. 0.0011; 0; Mismatches 9; | GTGGGAITGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA | V. V. |
| 25 33.6 53.3 300 3 US-C 26 33.6 53.3 1134 2 US-C 28 33.6 53.3 1134 2 US-C 29 33.6 53.3 1134 3 US-C 30 33.6 53.3 1143 3 US-C 31 33.6 53.3 1208 2 US-C 32 33.6 53.3 1416 3 US-C 32 33.6 53.3 1416 3 US-C 33 33.6 53.3 1416 3 US-C 34 33.6 53.3 1417 3 US-C 35 33.6 53.3 1417 3 US-C 36 33.6 53.3 1417 3 US-C 37 30.4 48.3 1993 3 US-C 38 30.4 48.3 1993 3 US-C 39 30.4 48.3 1993 3 US-C 42 27 42.9 174 2 US-C 43 27 42.9 174 2 US-C 44 26.6 42.2 133 3 US-C 45 25.6 40.6 185 3 U | Nicotiana tabacum 1-16 53.3% Similarity 81.2% 9; Conservative | 3GGATTGACGTGAGG 3GGATTGACGTGAGG | pplication US/08/402 MATION: Maliga, Pal Svab, Zora Staub, Jeffrey Scaubenko, Oleg Allison, Lori I Carrer, Helaine Kanevski, Ivan |
| C 26 33.6 53.3 300 3 US-09-202 C 27 33.6 53.3 1134 3 US-09-193 C 28 33.6 53.3 1134 3 US-09-193 3 3.6 53.3 1134 3 US-09-193 3 0 33.6 53.3 1208 2 US-08-193 3 3 3.6 53.3 1416 2 US-08-193 3 3 3.6 53.3 1416 3 US-09-193 C 34 33.6 53.3 1416 3 US-09-193 C 34 33.6 53.3 1417 3 US-09-193 C 34 33.6 53.3 1416 3 US-09-185 C 35 33.6 53.3 1416 3 US-09-187 C 40 30.4 48.3 7455 3 US-09-187 C 40 30.4 48.3 1993 3 US-09-187 C 40 30.4 48.3 7455 3 US-09-187 C 55 6 40.6 185 3 US-09-187 C 6 55 6 40.6 185 3 US-09-187 C 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | ; TYPE: DNA ; ORGANISM: Nic US-09-635-132-16 Query Match Best Local Simi | Oy 16 GTC Db 53 GTC | RESULT 2 18.08-198-256A-25 18.08-198-198-256A-25 19.08-198-198-256A-25 19.08-198-25-25-256A-25 19.08-25-25-25-25-25-25-25-25-25-25-25-25-25- |

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US/09/193,853
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APPLICANT: Maliga, Pal
                        ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 129 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 39; Conserv
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MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO US-09-193-853-25
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COUNTRY:
      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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US-09-193-853-25
US-09-193-853-25
Sequence 25, Application US/09193853
Fatent No. 6388168
GENERAL INFORMATION:
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Allison, Lori
APPLICANT: Allison, Lori
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: Transforming Plaetids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
TITLE OF SEQUENCES: 47
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TITLE OF INVENTION: DNA CONStructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 0.0011;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GTGGGATTGACGTGAGGGCAGGGATGGCTATATTTCTGGGAGCGAA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GTGGGATTGACGTGAGGGGCCTCCCTAGGCTATATTAGAGGGAGCGAA
                                                                                                                                             CUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLODEY/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 01-MAY-1999
FILING DATE: 01-MAY-1999
ATTORNEY/AGENT INPORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
FELECOMMUTCATION NUMBER: 36,252
TELECOMMUTCATION NUMBER: 36,252
TELECOMMUTCATION NUMBER: 36,252
TELECOMMUTCATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4104
TELEPAX: (215) 563-4104
INPORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 base pairs
NUMCHAIL 20 acid
NUMCHAIL 20 acid
NUMCHAIL 20 acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Dann, Dorfman, Herrell and Skillman
: 1601 Market Street Suite 720
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.3%;
Best Local Similarity 81.2%;
Matches 39; Conservative
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APPLICANT: Stab. Jose APPLICANT: Alison, Lori A. APPLICANT: Alison, Lori A. APPLICANT: Kanevski, Ivan APPLICANT: Kanevski, Ivan APPLICANT: Kanevski, Ivan TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Expressing Recombinant Proteins Therein NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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.larity 81.2%; Pred. No. 0.0011;
Conservative 0; Mismatches 9; Indels 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Thoppy disk
COMPUTER: PLOPPY disk
COMPUTER: PROFESTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/189,256A
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
ATTICNED ADTE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION:
TELEPHONE: (215) 563-4100
```

Gaps

```
APPLICANT: Svab, Zorra-
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Allson, Lori A.
APPLICANT: Allson, Lori A.
APPLICANT: Kanevski, Ivan
APPLICANT: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
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ADDRESSER: Dann, Dorfman, Herrell and Skillman STREBT: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08189256A
Patent No. 3877402
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
                                         REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4004
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    LENGTH: 140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 150 base pairs
nucleic acid
                 Reed, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO
US-09-193-853-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-189-256A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-Aug.-1993
PRIOR APPLICATION NUMBER: US 07/518,763
PRIOR APPLICATION NUMBER: US 07/518,763
FILING DATE: UL MAX-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4104
SEQUENCE CHARACTERISTICS:
FUNCTH: 140 base pairs
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FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Svab, Zora
Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
Kanevski, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.3'
Best Local Similarity 81.2'
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ջ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-189-256A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Svab, Deffrey
APPLICANT: Scaub, Jeffrey
APPLICANT: Scaub, Jeffrey
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: True or Invention: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
53.3%; Score 33.6; DB 2; Length 161;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #10, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A FILING DATE: 31-JAN-1994
FILING DATE: 31-JAN-1994
FILING APPLICATION DATA:
PROBLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PROR APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INPORMATION:
NAME: REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSER: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                Sequence 18, Application US/08189256A Patent No. 5877402 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
US-08-189-256A-18
                                                                                                                                                                                                 US-08-189-256A-18
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US-09-193-853-18
         Matches
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Patent No. 6388168

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Staub, Jeffrey

APPLICANT: Staub, Jeffrey

APPLICANT: Carrer, Helaine

APPLICANT: Allison, Lori A.

APPLICANT: Ranevski, Ivan

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Sulte 720

COUTY: Philadelphia
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                               Score 33.6; DB 3; Length 150; Pred. No. 0.0012;
                                                                                                                                                                      53.3%; Score 33.6; DB 2; Length 150;
81.2%; Pred. No. 0.0012;
tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                       16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION NUMBER: 0S 07/518,763
APPLICATION NUMBER: US 07/518,763
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: single
not relevant
E: DNA (genomic)
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81.2%;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genor
HYPOTHETICAL: NO
                                                                                                                                                                                                                       39; Conservative
                                                                                                                                                                                                 Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                     ; ANTI-SENSE: NO US-08-189-256A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-09-193-853-1
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Gaps

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TITLE OF INVENTION: DNA CONStructs and Methods for Stably
TITLE OF INVENTION: DNA CONStructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darn, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
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                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BEAGETIN BEAGE #1.0, Version #1.30
SOFTWARE: PELLOATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
FILING DATE: 31-JAN-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: CAPUG-1993
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: CAPUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: REED, JAN-1900
ATTORNEY/AGENT INFORMATION:
NAME: REED, JAN-1900
ATTORNEY/AGENT INFORMATION:
TELEBENOME: (215) 563-4100
TELEBENOME: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMPBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4104
INFORMATION FOR SEQ ID NO: 26.
SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1601 Marker
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                               USA
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US-08-189-256A-26
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-193-853-26
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                                                                                                                          APPLICANT: Stab, Joeffers
APPLICANT: Stab, Jeffers
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
ITILE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION .....
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECHOMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4104
; INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
'PMCTH: 161 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08189256A Patent No. 5877402 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Svab, Zora
Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.27
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-09-193-853-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-189-256A-26
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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STATE:
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Sequence 4, Application US/09193853

Sequence 4, Application US/09193853

Patent No. 6388168

GENERAL INFORMATION:
APPLICANT: Staub, Jeffrey
APPLICANT: Scubench, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: ALISON INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.3%; Score 33.6; DB 2; Length 165; 81.2%; Pred. No. 0.0012; Live 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 GTGGGATTGACGTGAGGGGCGCAGGATGGCTATATTTCTGGGAGCGAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
APPLICATION NUMBER: US/08/189,256A
PILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER/STICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , CLUOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-189-256A-4
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Best Local Similarity 81.2*
...rhes 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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CORRESPONDENCE ADDRESS: ATT CORRESPONDENCE ADDRESSE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 33.6; DB 3; Length 164; 81.2%; Pred. No. 0.0012; tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARR: Patentin Release #1.0, Version #1.30
                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION NUMBER: 03/518,763
APPLICATION NUMBER: 05/518,763
FILING DATE: 01-WAY-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPRA: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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Best Local Similarity
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; ANTI-SENSE: NO
US-09-193-853-26
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US-08-189-256A-4
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Gaps

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APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Joef V.
APPLICANT: Carrer, Helaine
APPLICANT: Anewski, Ivan
TITLE OF INVENTION: DNA CONSTRUCTS and Methods for Stably
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfe-
                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                       53.3%; Score 33.6; DB 2; Length 168; 81.2%; Pred. No. 0.0012; tive 0; Mismatches 9; Indels
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                        STRANDEDNESS: single
TOPOLGGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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not relevant
      nucleic acid
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nes 39; Conserv
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US-08-189-256A-2
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                                                                                                                                                                        Query Match
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APPLICANT: Stab, Jeffrey
APPLICANT: Stab, Jeffrey
APPLICANT: Stab, Jeffrey
APPLICANT: Carrer, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ind.
APPLICANT: Kanevski, Ind.
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
MARCHAN NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08189256A Patent No. 5877402 GENERAL INFORMATION:
                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
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SEQUENCE CHARACTERISTICS
F.RMCT...
                                                                                                                                                                                                                                                                                                                                                       Query Match 53.39
Best Local Similarity 81.2
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 base pairs
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APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103-2307
COMPUTER READABLE FORM:
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Best Local Similarity 81.2%; Pred. No. 0.0012; Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps

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Search completed: February 21, 2006, 05:40:12 Job time : 95 secs

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Sequence 14, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 15, Appl
Sequence 25, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 24, Appl
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952905,
952906,
693983,
13402, A
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                                                                         Pebruary 21, 2006, 05:41:51 ; Search time 410 Seconds
(without alignments)
326.188 Million cell updates/sec
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Sequence 1
Sequence 2
Sequence 2
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1: \( \cgn2_6 \) ptodata/1/\text{pubpna/USOB NEW PUB. seq:*} \)

2: \( \cgn2_6 \) ptodata/1/\text{pubpna/USOB NEW PUB. seq:*} \)

3: \( \cgn2_6 \) ptodata/1/\text{pubpna/USOB NEW PUB. seq:*} \)

4: \( \cgn2_6 \) ptodata/1/\text{pubpna/DEN TNEW PUB. seq:*} \)

5: \( \cgn2_6 \) ptodata/1/\text{pubpna/PET NEW PUB. seq:*} \)

6: \( \cgn2_6 \) ptodata/1/\text{pubpna/USOB NEW PUB. seq:*} \)

7: \( \cgn2_6 \) ptodata/1/\text{pubpna/USOB NEW PUB. seq:*} \)

7: \( \cgn2_6 \) ptodata/1/\text{pubpna/USIO NEW PUB. seq:*} \)

9: \( \cgn2_6 \) ptodata/1/\text{pubpna/USIO NEW PUB. seq:*} \)

10: \( \cgn2_6 \) ptodata/1/\text{pubpna/USII NEW PUB. seq:*} \)

11: \( \cgn2_6 \) ptodata/1/\text{pubpna/USII NEW PUB. seq:*} \)

12: \( \cgn2_6 \) ptodata/1/\text{pubpna/USII NEW PUB. seq:*} \)

13: \( \cgn2_6 \) ptodata/1/\text{pubpna/USII NEW PUB. seq:*} \)

13: \( \cgn2_6 \) ptodata/1/\text{pubpna/USII NEW PUB. seq:*} \)
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-190-122-3
US-11-190-122-1
US-11-190-122-1
US-11-190-122-1
US-11-527-048-15
US-10-527-048-25
US-10-527-048-24
US-10-527-048-24
US-10-527-048-24
US-10-527-048-24
US-10-925-065A-952906
US-09-925-065A-952906
US-09-925-065A-953933
US-10-995-561-13402
US-09-925-065A-753058
US-09-925-065A-308388
US-09-925-065A-308388
US-09-925-065A-308388
US-09-925-065A-308388
US-09-925-065A-308388
US-09-925-065A-308388
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                                                                                                                                                                                                                                   7204323 seqs, 1061406715 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Query
Match Length DB
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Perfect score:
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Maximum DB
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Sequence 539617, Sequence 539618, Sequence 519220, Sequence 36107, A Sequence 40865, A Sequence 67485, A Sequence 67485, A Sequence 67485, A Sequence 67485, A Sequence 8646, A Sequence 86646, A Sequence 86646, A Sequence 86646, A Sequence 86647, A Sequence 783808, Sequence 783808, 926199, 948723, 539617, 539618, Sequence Sequence US-09-925-065A-824462 US-11-072-512-1716 US-09-925-065A-513697 US-09-925-065A-948723 US-09-925-065A-539618 US-09-925-065A-539618 US-09-925-065A-539618 US-09-925-065A-36107 US-09-925-065A-36107 US-09-925-065A-36107 US-09-925-065A-40865 US-09-925-065A-48665 US-09-925-065A-64486 US-09-925-065A-64486 US-09-925-065A-864288 US-09-925-065A-86486 US-09-925-065A-86648 US-11-121-086-66 US-09-925-065A-783808 US-09-925-065A-705163 00000000 υ

ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA CHER INFORMATION: fragment codifying for the promoter region of the plastid 16S US-10-527-048-14
                          Sequence 14, Application US/10527048
Fublication No. US20060026704A1
GENERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology.
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC FLANTS.
TITLE REPERBURG: Vector for plastid transformation
CURRENT APPLICATION NUMBER: US/10/527,048
CURRENT FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
ILENGTH: 176
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Publication No. US20060031964A1
GENERAL INFORMATION:
APPLICANT: Daniell, Henry
ITILE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
FILE REFERENCE: CHL-T107C322
CURRENT APPLICATION NUMBER: US/11/190,122
CURRENT FILING DATE: 2005-07-25
PRIOR APPLICATION NUMBER: 60/344,704
PRIOR FILING DATE: 2001-12-26
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                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 39; Conserv
US-10-527-048-14
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US-11-190-122-3
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753057

Gaps

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US-11-190-122-2

Publication No. US20060031964A1

GENERAL INFORMATION:

GENERAL INFORMATION:

FILE REFERENCE GHI-TJ070222

FILE REFERENCE:

GURRENT PILING DATE: 2005-07-25

CURRENT PILING DATE: 2001-12-26

FRIOR APPLICATION NUMBER: 05/344,704

PRIOR APPLICATION NUMBER: 05/344,704

PRIOR APPLICATION NUMBER: 05/30,021157

FRIOR APPLICATION NUMBER: 05/50,351

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-07-03

PRIOR APPLICATION NUMBER: 60/590,848

PRIOR FILING DATE: 2004-07-23

PRIOR FILING DATE: 2004-07-23

PRIOR PELING DATE: 2002-03

PRIOR APPLICATION NUMBER: 60/490,816

PRIOR PELING DATE: 2002-03

PRIOR PELING DATE: 2002-07-03

PRIOR
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TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
FILE REFERENCE: Vector for plastid transformation
CURRENT APPLICATION NUMBER: US/10/527,048
CURRENT FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                            Length 2800;
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                                                                                                                                                                                                                                  Indels
                                                                                                                                                Score 33.6; DB 9;
Pred. No. 0.004;
0; Mismatches 9;
       ; FEATURE:
; OTHER INFORMATION: aadA/BADH expression cassette
US-11-190-122-1
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US-11-190-122-2
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                                                                                                                                                            53.3%;
81.2%;
                                                                                                                                                                                                                                  39; Conservative
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Best Local Similarity
Matches 39; Conserv
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TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
FILE REFERENCE: CHL-T10/5122
CURRENT APPLICATION NUMBER: US/11/190,122
CURRENT FILING DATE: 2005-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PRIOR APPLICATION NUMBER: 60/344,704
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/590,848
PRIOR APPLICATION NUMBER: 60/590,848
PRIOR PILING DATE: 2004-07-23
PRIOR PELING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/400,816
PRIOR PILING DATE: 2002-09-02
PRIOR APPLICATION NUMBER: 60/393,651
PRIOR PILING DATE: 2002-09-03
PRIOR PILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/393,428
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 10/500,351
PRIOR PILING DATE: 2004-06-25
PRIOR PELING DATE: 2004-06-25
PRIOR PILING DATE: 2003-07-03
PRIOR FILING DATE: 2003-07-03
PRIOR PILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/590,751
PRIOR APPLICATION NUMBER: 60/590,751
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-10-30
PRIOR FILING DATE: 2002-08-02
PRIOR PILING DATE: 2002-08-02
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-12-26
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Publication No. US20060031964A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 2569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: ARTIFICIAL
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US-11-190-122-1
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Gaps

Gaps

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63

Length 6659;

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16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
       Score 33.6; DB 7; Length 6
Pred. No. 0.0045;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                            Sequence 24, Application US/10527048
Publication No. US20060026704A1
GENERAL INFORMATION:
         53.3%;
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66.1%;
                               Best Local Similarity 81.2
Matches 39; Conservative
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            Query Match
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                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA OTHER INFORMATION: fragment from the vector pVTPA between the rice atpB and OTHER INFORMATION: tobacco rbcL borders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA OTHER INFORMATION: fragment from the vector pVTPA-Bar between the rice atpB and OTHER INFORMATION: tobacco rbcL borders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Center for Genetic Engineering and Biotechnology.
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
FILE REFERENCE: Vector for plastid transformation
CURRENT APPLICATION NUMBER: US/10/527,048
CURRENT FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 6465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/10527048
Publication No. US20060026704A1
Publication No. US20060026704A1
SEGNERAL INFORMATION:
APPLICANT: Center for Genetic Engineering and Biotechnology.
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
FILE REPERENCE: Vector for plastid transformation
CURRENT APPLICATION UNMER: US/10/527,048
CURRENT APPLICATION UNMER: 2005-03-07
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 6659
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                                                                                                                                                                                                                                                     ch 53.3%; Score 33.6; DB 7; Length 5834; l Similarity 81.2%; Pred. No. 0.0044; 39; Conservative 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                    16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
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Pred. No. 0.0044;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/10527048
Publication No. US20060026704A1
GENERAL INFORMATION:
                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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81.2%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.2
Matches 39; Conservative
                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                           ; US-10-527-048-15
                                                LENGTH: 5834
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                                                                                                                    FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DN. OTHER INFORMATION: fragment from the vector pVTPA-HB-aadA between the rice atpB. OTHER INFORMATION: tobacco rbcL borders.
APPLICANT: Center for Genetic Engineering and Biotechnology.
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
TITLE REFERENCE: Vector for plastid transformation
CURRENT APPLICATION NUMBER: US/10/527,048
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: Identification and Mapping of Single
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    FILE REPRENCE: 108827.135
    CURRENT APPLICATION NUMBER: US/09/925,065A
    CURRENT FILING DATE: 2001-08-08
    PRIOR APPLICATION NUMBER: US 60/243,096
    PRIOR APPLICATION NUMBER: US 60/252,147
    PRIOR APPLICATION NUMBER: US 60/250,092
    PRIOR APPLICATION NUMBER: US 60/261,766
    PRIOR APPLICATION NUMBER: US 60/261,766
    PRIOR APPLICATION NUMBER: US 60/261,766
    PRIOR FILING DATE: 20001-01-16
    PRIOR FILING DATE: 20001-01-16
    PRIOR FILING DATE: 2001-01-16
    PRIOR FILING DATE: 2001-01-16
    PRIOR FILING DATE: 2001-01-16
    PRIOR FILING DATE: 2001-05-09
    NUMBER OF SEQ ID NOS: 957086
    SEQ ID NO 935299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
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Pred. No. 3.5;
0; Mismatches 19;
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Best Local Similarity 66.1
Matches 37; Conservative
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SEQ ID NO 693983
LENGTH: 624
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Sequence 952905, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVERTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILIATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR PLILING DATE: 2000-11-30

PRIOR PLILOGATION NUMBER: US 60/250,766

PRIOR FILING DATE: 2001-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2010-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 935300
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Pred. No. 3.5;
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40.6*; Score 25.6; DE
Best Local Similarity 66.1*; Pred. No. 3.5;
Matches 37; Conservative 0; Mismatches
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Publication No. US20040181048A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-925-065A-952905
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; ORGANISM: Homo sapiens
US-09-925-065A-935300
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Length 562;

DB 6;

Score 25.6;

40.68;

Query Match

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                                                        0; Gaps
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Publication No. US20040181048A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single |
| TITLE OF INVENTION: Identification and Mapping of Single |
| TITLE OF INVENTION: Identification and Mapping of Single |
| TITLE REFERENCE: 108827.115 |
| CURRENT APPLICATION NUMBER: US/09/925,065A |
| PRIOR PILING DATE: 2000-10-24 |
| PRIOR FILING DATE: 2000-11-20 |
| PRIOR FILING DATE: 2000-11-20 |
| PRIOR FILING DATE: 2000-11-30 |
| PRIOR FILING DATE: 2000-11-30 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR FILING DATE: 2010-01-16 |
| PRIOR FILING DATE: 201
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome;
FILE PEPERENEE: 108027.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR PELING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR PELING DATE: 2000-11-30
FRIOR FILING DATE: 2001-11-30
FRIOR FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR FILING DATE: 2001-01-16
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                                                        19; Indels
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Pred. No. 3.5;
0; Mismatches 19;
Best Local Similarity 66.1%; Pred. No. 3.5; Matches 37; Conservative 0; Mismatches
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Best Local Similarity 66.1%;
Matches 37; Conservative
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US-09-925-065A-952906
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US-09-925-065A-693983
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; LOCATION: (1)...(56054)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13402
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDICASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION:
TITLE OF INVENTION: CARDICASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILLING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FEBELSEQ for Windows Version 4.0
SEQ ID NO 13402
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JULIACEART: Wang, David G.
JULIACEART: WANGSTON: Nucleoctide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925.065A
CURRENT FILING DATE: 2000-10-8-08
PRIOR APPLICATION NUMBER: US 60/243.096
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
SEQ ID NO 753058
JENGRAF: 541
LENGRAF: 541
TVPE: DAN
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                                                 Score 25.6; DB 6; Length 624;
Pred. No. 3.5;
0; Mismatches 19; Indels (
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                                            40.6%;
Best Local Similarity 66.1%;
Matches 37; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-925-065A-753058
US-09-925-065A-693983
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US-09-925-065A-753058
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US-10-995-561-13402
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Gaps
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0
   DB 6; Length 561;
 38.4%; Score 24.2; DB 6; Length 56 66.0%; Pred. No. 12; Live 0; Mismatches 18; Indels
Query Match
Best Local Similarity 66.09
Matches 35; Conservative
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Search completed: February 21, 2006, 06:33:19 Job time : 411 secs

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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

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Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Pal Maliga
APPLICANT: Don Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
FILE REFERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: US/10/737,251
CURRENT APPLICATION NUMBER: 60/433,302
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR PILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-737-251-18
Sequence 18, Application US/10737251
Sequence 18, Application No. US20040221338A1
GENERAL INFORMATION:
APPLICANT: Pal Mailga
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression;
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
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Sequence 43,
Sequence 1, A
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Pred. No. 2.6e-15;
; Mismatches 0;
US-10-460-716-3

US-10-473-207-26

US-10-473-207-26

US-10-30-27-25

US-10-680-824A-1

US-10-680-824A-2

US-10-680-824A-2

US-10-680-824A-2

US-10-680-824A-1

US-10-680-824A-1

US-10-957-562-4

US-10-957-562-4

US-10-737-251-11

US-10-737-251-11

US-10-737-251-11

US-10-109-812-4

US-10-109-812-4

US-10-109-812-4

US-10-28-253-16

US-10-109-812-4

US-10-109-812-4

US-10-109-812-4

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US-10-109-812-1
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Publication No. US20040221338A1
GENERAL INFORMATION:
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Gaps

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Length 112;

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APPLICANT: Pal Maliga
APPLICANT: Pal Maliga
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
FILE REFERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: US/10/737,251
PURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR PILING DATE: 2002-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication Wo. US20040221338A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pal Mailga
APPLICANT: DON Y. Suzuki
APPLICANT: Pal Mailga
APPLICANT: DON Y. Suzuki
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
FILE REFERENCE: 1594 RUT 03-083US
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR FILING DATE: 2002-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GAGGTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
                                                                                                                                                                                                                                                                                                                                      58.1%; Score 36.6; DB 8; Length 112; 82.4%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
                                                                                                                                                                                               ch 61.0%; Score 38.4; DB 8; 1 Similarity 87.5%; Pred. No. 2.2e-05; 42; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                  ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 51
SOFTWAREE FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 112
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SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 10, Application US/10737251
; Publication No. US20040221338Al
; GENERAL INFORMATION:
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                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Matches 42; Conserv
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Matches 42; Conserv
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US-10-737-251-9
                          LENGTH: 112
SEQ ID NO 23
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APPLICANT: Jon Y. Suzuki
APPLICANT: Jon Y. Suzuki
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: CONSTRUCTION of Chimeric Promoters for Transgene Expression
FILE REPERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: 03/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR PILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PSECSEQ for Windows Version 3.0
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/10737251
; Sequence 23, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Dlastid rRNA Operon PromoterElements for
TITLE OF INVENTION: CONSTRUCTION OF CURRENT PRPLICATION NUMBER: US/10/737,251
; CURRENT PELLING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.4; DB 8; Length 112;
Pred. No. 2.2e-05;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                61.0%; Score 38.4; DB 8; Length 112; 87.5%; Pred. No. 2.2e-05; cive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 GTGGGATTGACGTGAGGGGCTCCGATGGCTATATTTCTGGGGGCGAA
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                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Prrn promoter derivative US-10-737-251-18
FILE REFERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 19, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 61.0%;
| Similarity 87.5%;
| 42; Conservative
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                            SEQ ID NO 18
LENGTH: 112
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APPLICANT: PAI MAIJGA
APPLICANT: PAI MAIJGA
APPLICANT: PAI MAIJGA
APPLICANT: JON Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Onstruction of Chimeric Promoters for Transgene Expression
FILE REPERBNCE: 1594 RUT 03-083US
CURRENT PAPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR PILING DATE: 2003-12-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
28 GTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-5
                                                                                       US-10-737-251-5
; Sequence 5, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 81.2%;
Matches 39; Conservative (
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US-10-737-251-6
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LENGTH: 112
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Sequence 3, Application US/10737251

Sequence 3, Application US/10737251

Sequence 3, Application No. US20040221338A1

SENBEAL INFORMATION:

APPLICANT: Pal Maliga
APPLICANT: Pal Maliga
APPLICANT: Pal Maliga
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: DATE: 2003-183.80

FILE REFRENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: 06/433,302

PRIOR APPLICATION NUMBER: 60/433,302

PRIOR FILLING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Pal Maliga
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid RNA Operon PromoterElements for
TITLE OF INVENTION: Plastid RNA Operon Promoters for Transgene Expression
TITLE OF INVENTION: Oracle 103-083US
CURRENT APPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR SEQ ID NOS: 51
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 112
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                                                                                                                   63
                                                                                                                                     22 TCCCTCGTGGGATTGACGTGAGGGGGGGGAGGCTATATTCTGGGAGCGAA 75
                                                                                                         10 TCCGAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
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          Query Match
55.2%; Score 34.8; DB 8; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.00064;
Matches 42; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%; Score 33.6; DB 8; Length 112; llarity 81.2%; Pred. No. 0.0019; Conservative 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 GTGGGATTCACGTGAGGGGAGGGATGGCTATATTCTCGGAGCGAA 75
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81.2%; Pred. No. 0.0019;
iive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-3
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Publication No. US20040221338A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.27
Matches 39; Conservative
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Best Local Simi]
Matches 39; (
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8; Length 112;

Score 33.6; DB 8; Length 11 Pred. No. 0.0019; 0; Mismatches 9; Indels

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Sequence 6, Application US/10737251
Publication No. US20040221338A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pal Maliga
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid TRNA Operon PromoterElements for TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression; TITLE OF INVENTION: PLASTICALION OF CHIMERER US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR PAPLICATION NUMBER: 60/433,302
PRIOR PLILING DATE: 2002-12-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.3%; Score 33.6; DB 8; Length 112; Best Local Similarity 81.2%; Pred. No. 0.0019; Matches 39; Conservative 0; Mismatches 9; Indels
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; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-6
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; Publication No. US20040221338A1
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16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA

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PRIOR APPLICATION NUMBER: 60/433,302 PRIOR FILING DATE: 2002-12-13
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Publication No. US20040221338A1

GENERAL INFORMATION:

APPLICANT: Pal Mailga

TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
FILE REPRENCE: 1594 RUT 03-083US

CURRENT APPLICATION NUMBER: US/10/737,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dai Maliga
APPLICANT: Don Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression
FILE REFERENCE: 1594 RUT 03-083US
CURRENT PEPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastEEQ for Windows Version 3.0
SEQ ID NO 8
                 APPLICANT: Pal Maliga
APPLICANT: Pal Maliga
APPLICANT: Jon Y. Suzuki
TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression
FILE REFERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR FILING DATE: 2002-12-13
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Pred. No. 0.0019;
0; Mismatches 9; Indels
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53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-8
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-7
                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10737251 Publication No. US20040221338A1 GENERAL INFORMATION:
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81.2%;
                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Matches 39; Conservative
GENERAL INFORMATION:
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Sequence 28, Application US/10737251

Sequence 28, Application US/10737251

Publication No. US20040221338A1

GENERAL INFORMATION:

APPLICANT: Pal Maliga

APPLICANT: Pal Maliga

TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression

TITLE OF INVENTION: D1831 O18318

TITLE OF INVENTION: 0.08318

CURRENT FILING DATE: 2003-12-15

CURRENT FILING DATE: 2003-12-15

PRIOR PILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 28

LENTING DATE: 112
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Sequence 29, Application US/10737251

Publication No. US20040221338A1

SENERAL INFORMATION:

APPLICANT: Pal Maliga

APPLICANT: Joh X. Suzuki

TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression

TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression

TITLE REFERENCE: 1594 RUT 03-0830S

CURRENT FILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US/10/737,251

CURRENT FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.6; DB 8; Length 112;
pred. No. 0.0019;
0; Mismatches 9; Indels (
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                                                                                                                                                                                                                                                             Query Match 53.3%; Score 33.6; DB 8; Length 112; Best Local Similarity 81.2%; Pred. No. 0.0019; Matches 39; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                      16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
                                                                                                                                                                     ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Prrn promoter derivative US-10-737-251-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 112
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81.2%;
                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 81.2
Matches 39; Conservative
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BOMAG13TR

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B2440851 B245817 B2476817 B2470963 B4240802 BH430502 BH630640 BH43122 BH620640 BH43122 BH620640 BH4349701 BH64090 BH64090 BH64090 BH64090 BH64090 BH64090 BH64090 BH64090

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LERJE32TR BOMGJ20TR BOOAT93TR BOGOO69TF

BOMFU26TR BOIFK28TF

BH657205 CC966698 BZ447238 BH543946

BZ447238 BH543946 BH657205 CC966698

BH678091

ALIGNMENTS

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CN872595 020807AAP
AJ876197 AJ876197
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BZ483881 BOOAL39TR
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BH677595 BOMCM49TR
BH588286 BOGFU54TF
                                         February 21, 2006, 05:37:59; Search time 3773 Seconds (without alignments) 781.231 Million cell updates/sec
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                                                                                  1 gagctcttctccgaggtggg......gctatatagagggagcgaa 63
                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                 82156650
    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                  41078325 segs, 23393541228 residues
                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                                                                                                              Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                              OM nucleic - nucleic search, using sw model
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AJ876197
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                   US-10-737-251-51
63
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gb_est2::
gb_est2::
gb_htc::
gb_est4::
gb_est5::
gb_est5::
gb_est7::
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gb_gss1::
gb_gss2::
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Match Length
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| RESULT 1 BH009665/ LOCUS DEFINITIO ACCESTON VERNORDS SOURCE ORGANIS! TITLE JOURNAL COMMENT FEATURES SOUR | υ | | ef31f05.x1 TO1000 Brassic genomic survey sequence. | BH009665 | BH009665.1 GI:13955602 GSS. | | M Brassica oleracea Rukarvota: Viridinlantae: Strentonhyta: Rmhrvonhyta: Tranhoonhyta: | Spermatophyta; Magnoliophyta; endicotyledons; core endicotyledons; | | | Miller B. Nascimento I. Preston B. Rodricnez S. Santos I. | Shah. R. Vil. M. D. Zutavern T. Bal. H. Dedhia N. and McCombie W. R. | Whole Genome Shotgun Reads from Brassica oleracea | | Contact: W. Richard McCombie | Lita Annenberg Hazen Genome Sequencing Center | Cold Spring Harbor Laboratory | PO Box 100, Cold Spring Harbor, NY 11/24, USA | 516 367 | Fax: 516 367 8874 | - 5 | Plate: ef31 row: f column: 05 | Seg primer: -21fwdUniv | crass: shocgun | High quality sequence stop: 243. | | - | /organism="Brassica Oleracea" | (mol_type="genomic DNA" | /db_xret="taxon:3712" | /clone="ef31f05" | /clone_lib="TO1000" | /note="Vector: M13 for .x reads, pZero-2 for .b and .g | reads; Site_1: EcoRV; DNA prepared as whole genome shotgun | library from young, green leaves. May contain some plastid | UNAS. DNA provided by Dr. Tom Osborn, University of | Wisconsin-Madison, Department of Agronomy." | |
|--|------------------------|-------|--|-----------|--------------------------------|--------|---|--|-----------|---------|---|--|---|---------|------------------------------|---|-------------------------------|---|---------|-------------------|-----|-------------------------------|------------------------|----------------|----------------------------------|----------|--------|-------------------------------|-------------------------|-----------------------|------------------|---------------------|--|--|--|---|---|--------|
| | RESULT 1 BH009665/C | rocus | DEFINITION | ACCESSION | VERSION | SOURCE | ORGANISM | | REFERENCE | CNOTTON | | | TITLE | JOURNAL | COMMENT | | | | | | | | | | | FEATURES | sonrce | | | | | | | | | | | ORIGIN |

BOGQI49TF

AQ962945 BH537952 BH677595 BH588286

444444444

BZ507339

AQ962940 BZ483881

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BH474703 I BZ507339 I DT034079 V BH646726 I

DEFINITION

LOCUS

RESULT 2 BZ457960

ò g ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

PUBMED COMMENT

FEATURES

JOURNAL

TITLE

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BOWDD83TR BO_2_3 KB Brassica oleracea genomic clone BOMDD83, genomic survey sequence.
BH678911
GSS 19-FEB-2002
BH678911.1 GI:18749354
GSS.
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y. Hortkesearch Apple EST Project
Unpublished Apple EST Project
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
Tel. 00 64 09 815 4200
Fax: 00 64 09 815 4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica oleracea
Brassica oleracea
Brusryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 395)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and and anotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
                                                                                                                                                                                                                                 /note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BOMDDB3"
-Clone lib=="BO_23 KB"
-/note="Vector: pHGSI; Site_1: BstXI; 2-3 kb sheared
-/note="Vector: pHGSI; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHGSI using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: Stap primers and Class sheared ends.
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Tel: 301-838-3523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
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COMMENT
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COMMENT
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         AUTHORS
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BH678911
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KEYWORDS
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                                                                                                                                                                                                                                                              BZ457960 295 bp DNA linear GSS 13-DEC-2002 BONDT72TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDT72,
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Malus x domestica
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids 1, Rosales, Rosaceae; Maloideae, Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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total DNA inserted into pHŌS1 using BstXI linkers"
                                                     Gaps
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Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
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Tel: 301-838-3523
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                                                     10; Indels
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         50.8%; Score 32; DB 9 79.2%; Pred. No. 1.1; ive 0; Mismatches
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chris Town
Ouery Match
Best Local Similarity 79.2'
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea
Brassica oleracea
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RESULT 3 CN859023

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VERSION KEYWORDS

ORGANISM

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Gaps

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LOCUS DEFINITION

RESULT 5 CN930271

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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McArtney, D., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y. Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after bloom Prunus persica cDNA clone PR0213A05, mRNA sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Rosales, Rosaceae, Amygdaloideae, Prunus.
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/clone_lib="Prunus persica fruit mesocarp plus epidermis
80 days after bloom"
                                                                                                                                                                            Zealand Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                           /issue_rangoring.
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/note="Vector: pBK-CWV; Library sequenced by Genesis
Research & Development"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                         Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Fax: 00 64 09 815 4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.8%; Score 32; DB 7; Length 498; ilarity 79.2%; Pred. No. 1.1; Conservative 0; Mismatches 10; Indels
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Urefv, Inra, INRA, Centre de Bordeaux
BP 81 Villenave d'Ornon Cedex, 33 883, FRANCE.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                      /organism="Malus x domestica"
|mol type="mRNA"
|do xref="taxon:3750"
|clone="AAPA005328"
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1 Similarity 79.2%; Pred. No. 1.1;
38; Conservative 0; Mismatches
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/organism="Prunus persica"
                                                                                                                                                                                                                                                                 Email: est@hortresearch.co.nz.
Location/Qualifiers
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                1. .498
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Best Local Similarity
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Best Local Similarity
Matches 38; Conserv
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                                                                           TITLE
JOURNAL
COMMENT
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                                    AUTHORS
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KEYWORDS
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Malus x domestica
Malus x domestica
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

I (bases I to 415)
S Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McAttney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
L Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
                                                                                                                                                                                                                                                                                                                                 CN930271 415 bp mRNA linear EST 07-JUN-2004 000322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA clone AFBC002396, mRNA sequence.
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/organism="Malus x domestica"
/mol_type="RRMN:"
/db_xref="taxon:"3750"
/clone="AFBC002396"
/tissue_type="Floral bud"
/dev_stage="Pre-opening, flower at stage of nectar/pollen
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Malus x domestica
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids; eurosids I; Rosales; Rosaceae, Maloideae, Malus.
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/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"
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                                                                             Length 395;
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                                                                                                                         10; Indels
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                                                                        DB 9;
                                                                        Score 32; DB 9;
Pred. No. 1.1;
0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           CN930271.1 GI:48403084
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                                                                      50.8%;
                                                                 Query Match
Best Local Similarity 79.2'
Matches 38; Conservative
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source

FEATURES

Query Match Best Local

Matches

8 В DEFINITION

RESULT 6 CN872595

ACCESSION

VERSION KEYWORDS

ORGANISM

REFERENCE

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Gaps

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Gaps

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CG026772 734 bp DNA linear GSS 19-AUG-2003 PGAAB74TR PGAA Carica papaya genomic clone PGAAB74, genomic survey
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Carica papaya
Carica papaya
Carica papaya
Carica papaya
Carica papaya
Carica papaya
Spermatophyta, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids; eurosids II; Brassicales; Caricaceae, Carica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA provided by Ray Ming was isolated from cultivar SunUp that was
trasngenic for papaya ringspot virus coat protein gene
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
Contact: Gleave, A.
Sequencing Facility
Sequencing Facility
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Ltd
121 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
                                                                                                                                                                                                                                        | ... 598 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 
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/mol_type="genomic DNA"
/cultivarabungh
/db xref="taxon:3649"
/clone="PGAAB74"
/clone="PGAAB74"
/note="PGAAB74"
/note="PGAAB74"
/note="PGAAB74"
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Carica papaya Unpublished (2003)
Other GSSs: PGAAB14TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.8%; Score 32; DB 7; Length 598; 79.2%; Pred. No. 1.1; ive 0; Mismatches 10; Indels
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Matches 38; Conservative
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Fax: 301-838-0208
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KEYWORDS
SOURCE
ORGANISM
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CG026772/c
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AUTHORS
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Malus x domestica
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 598)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
Unpublished (2004)
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Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Dases I to S61)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Fax: 301-838-3523
Fax: 301-838-0208
Email: cdtcwn@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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/organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO1000bH3"
/db_xref="taxon:3712"
/clone="BOGRW45"
                                                                                                                                                                                                                                                                                                               BH522564.1 GI:17730649
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Contact: Chris Town
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Best Local Similarity 79.2%;
Matches 38; Conservative (
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AQ962940 linear GSS 28-JAN-2000 LERGI42TR LERG Arabidopsis thaliana genomic clone LERGI42, genomic
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/clone="LERG142"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was
sheared to 0.4-0.7 Kbp before ligation."
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 169)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
                                                                                                                                                                                                                                                                                                                                                  /db_xrefe="taxon:3712"
/clone="BONLE31"
/clone="BONLE31"
/note="Vector: pHoS1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHoS1 using BstXI linkers"
                                                                                                            Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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                                                                                            9712 Medical Center Drive, Rockville, MD 20850,
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                                                                                                                                                                                                                                                                                      /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, I
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
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/ecotype="Landsberg erecta"
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GSS.
                         Other_GSSs: BONLE43TR
Contact: Chris Town
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Unpublished (2000)
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Class: shotgun.
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Best Local Similarity
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Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Caricaceae; Carica.
I (basea I to 764)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Carica papaya
Other GSSs: PGAAR3OTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org

DNA provided by Ray Ming was isolated from cultivar SunUp that was

transgenic for papaya ringspot virus coat protein gene

Seq primer: TP

Class: sheared ends.
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Warayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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/mol_type="genomic DNA"
/cultivar="SunUp"
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/clone="PGAAE30"
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BZ498361.1 GI:27012539
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Fax: 301-838-0208
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MD 20850, USA

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Search completed: February 21, 2006, 07:16:42 Job time : 3776 secs
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hes 37; Conserv
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LERGI45TR LERG Arabidopsis thaliana genomic clone LERG145, genomic
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Brusaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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/strain="TO100DH3"
/db xref="texon:3712"
/clone="BOOA129"
/clone="BOOA129"
/clone="BOOA129"
/clone="boOA129"
/clone="boOA129"
/clone="texon: phoO31; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into phOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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                                                                                               Email: cdcown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: Seq primer: Class: Sheared ends.
Location/Qualifiers
                                                                             16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
Score 30.4; DB 9; Length 169;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GTGGGATTGACGTGAGGGGCCTCCCTAGGCTATATTAGAGGGAGCGAA
                                       11;
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/organism="Brassica oleracea"
                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other GSSs: BOOAI29TF
Contact: Chris Town
   Query Match
Best Local Similarity 77.1%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                           Brassica oleracea
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Fax: 301-838-0208
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Matches 37; Conserv
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SOURCE
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COMMENT
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KEYWORDS
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/mol_type="genomic_DNA"
/mol_type="genomic_DNA"
/db xref="landsberg erecta"
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/note="Organ - Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."
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                    1 (bases 1 to 194)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Belblyum, T., Liang, P., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                          polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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    194
/organism="Arabidopsis thaliana"

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                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: TR
Class: shotgun.
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February 21, 2006, 05:33:20 ; Search time 282 Seconds (without alignments) 1488.921 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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63
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6: genesegn2001as:*
7: genesegn2003as:*
9: genesegn2003as:*
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| r0 | Description | Adt78252 Mutant Pr | Adt78220 DNA seque | Adt78224 DNA seque | Adt78219 DNA seque | Adt78211 DNA seque | Adt78210 DNA seque | Acc85363 N tabacum | Ade34206 Tobacco P | Adt78229 DNA seque | Adt78231 DNA seque | Adt78228 DNA seque | Adt78230 DNA seque | Adt78207 DNA seque | Adt78204 DNA segue | Adt78208 DNA seque | Adt78206 DNA seque | Adt78205 DNA seque | Adt78209 DNA seque | Aea36357 Oligonic |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| SUMMARIES | Ω | ADT78252 | ADT78220 | ADT78224 | ADT78219 | ADT78211 | ADT78210 | ACC85363 | ADE34206 | ADT78229 | ADT78231 | ADT78228 | ADT78230 | ADT78207 | ADT78204 | ADT78208 | ADT78206 | ADT78205 | ADT78209 | AEA36357 |
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| | % Query Match Length DB | 63 | 112 | 112 | 112 | 112 | 112 | 91 | 91 | 112 | 112 | 112 | 112 | 112 | 112 | 112 | 112 | 112 | 112 | 113 |
| , | & Query Match | 100.0 | 61.0 | 61.0 | 61.0 | 58.1 | 55.2 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 |
| | Score | 63 | 38.4 | 38.4 | 38.4 | 36.6 | 34.8 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 |
| | Result No. | н | 7 | m | 4 | 2 | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences

Claim 7; SEQ ID NO 51; 34pp; English.

New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

| Additional Additional Pastid 1 21424 | ADX117 AADX117 AAAX214 | 19 14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 53.3 119 14 53.3 127 4 53.3 129 2 53.3 129 2 53.3 140 2 53.3 142 6 53.3 166 2 53.3 168 2 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 168 4 53.3 184 4 53.3 244 4 | 53.3 53.3 53.3 53.3 53.3 53.3 53.3 53.3 | 1.6 53 1.6 53 1.7 53 1.7 53 1.8 53 | 1 33.6 3 3.6 3 3.6 3 3.6 5 33.6 6 33.6 9 33.6 1 33.6 1 33.6 1 33.6 1 33.6 1 33.6 2 33.6 2 33.6 2 33.6 2 33.6 2 33.6 3 33.6 4 33.6 2 33.6 2 33.6 4 33.6 2 33.6 4 33.6 2 33.6 6 33.6 6 33.6 6 33.6 6 33.6 7 33.6 7 33.6 7 33.6 8 33. | 20 21 22 22 23 23 24 24 33 33 33 33 33 33 33 33 33 33 33 33 34 44 4 | A S S S S S S S S S S S S S S S S S S S | |
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| PTME; chimeric promoter; mutant | expressi og elemer | yene Jatir | transon modu | lant; | ic p | ansgeni rn trar | T I | ¥ | |
| and the state of t | | 3 | | | · . | 1000 | î | × | |
| for transgene expression | | rrn1] | | окошс | | | M | Z E | |
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| | ЗР. | | | ndard | sta | 1 2 T78252 | ULT 7825 AD | RESI ADT | |
| MENTS | ALIGN | | | | | | | | |
| Aat85195 Plastid | AAT85195 | 7 | 1134 | 53.3 | | | | U | |
| Aax21429 Regulato Ade34327 Vector | AAX21429 ADE3432 | 10 | 258 804 | 53.3 | | | | | |
| Aaf57903 | AAF5790 | 41 | 244 | 53.3 | | | 27 | | |
| Aaz88176 Aa£25353 | AAZ88176 AAF25353 | W 4 | 2 4 4 2 4 4 | 53.3 53.3 | | | 40 | | |
| Aaa47372 Prrn/NEI | AAA47372 | 3 | 244 | 53.3 | | | 39 | | |
| Adt/8243 Tobacco Adt/8243 Carrot | ADT 7824 | 7 5 | 234 | . e. | | | 38 | | |
| Abs54934 DNA seque | ABS54934 | 9, | 220 | 53.3 | | | 36 | | |
| Aa189143 Aat66301 | AAF6514 | 4 0 | 201 | 53.3 | | | 3 t | | |
| Admo1282 Plastid | ADM0128 | 12 | 176 | 53.3 | | | 33 | | |
| Aai25352 Aai57902 | AAF57902 | 4.4 | 168 | 53.3 | | | 32 | | |
| Aaz88175 | AAZ88175 | m s | 168 | 53.3 | | | 30 | | |
| Aax21407 | AAX21407 | 10 | 168 | 53.3 | | | 53 | | |
| Aax21431 Aax21409 | AAX21431 | 7 0 | 165 | 53. t | | | 7 8 7 | | |
| Aax21423 | AAX21423 | 0 C | 161 | 53.3 | | • | 26 | | |
| Aax21406 | AAX21406 | 0 0 | 150 | 53.3 | | • | 25 | | |
| A4X21424 Ab555361 | ABS55361 | 9 9 | 142 | 53.5 | | | 24 | | |
| Aax21430 Regulat | AAX2143(| 01 (| 129 | 53.3 | 10.14 | 33.6 | 22 | | |
| Adf84276 Plastid 1 | AAF84276 | -1 -4- 14 | 127 | 53.5 | 0 10 | 33.6 | 21 | | |
| 000 top4 | 2071704 | - | 0.5 | , | u | , , , | Ċ | | |

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mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID Nos: 31. Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this ruccio; (c) a chimeric promoter for expression of transgenes in plastids of thigher plants, comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a promoter being further operably linked to a sequence encoding a chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule of interest or its precursor. C relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins expression and for driving high level expression of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in plastids. The present sequence represents a mutant Prrn promoter that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used to express heterologous molecules in the plastids of higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plants
              8888888888888888888888888888888888
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Sequence 63 BP; 13 A; 12 C; 24 G; 14 T; 0 U; 0 Other;

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                                                  1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGC
                                                                1 GAGCTCTTCTCCGAGGTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGC
                           Gaps
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 Length 63;
                       Indels
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100.0%; Score 63; DB 13; 100.0%; Pred. No. 8.1e-14;
                         0; Mismatches
                         63; Conservative
            Best Local Similarity
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DNA sequence of Prrn promoter derivative pJYS172. ADT78220 standard; DNA; 112 BP. (first entry) 27-JAN-2005 ADT78220: RESULT 2

Heterologous molecule expression; plastid rRNA operon; Prrn promoter;

transgenic plant; transgene expression; Prrn transcription modulating element; PTME; chimeric promoter; ds.

Unidentified

US2004221338-A1.

04-NOV-2004.

13-DEC-2002; 2002US-0433302P.

15-DEC-2003; 2003US-00737251

(MALI/) MALIGA P. (SUZU/) SUZUKI J Y.

Suzuki JY; Maliga P,

WPI; 2004-774976/76.

New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

Claim 1; SEQ ID NO 19; 34pp; English

e invention relates to nucleic acid sequences for promoting expression heterologous molecules in the plastids of higher plants. The nucleic

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acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-10 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the complete acid sequence above. (b) a transgenic plant comprising the complete acid sequence above. (b) a transgenic plant comprising this vector. (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating complement (PTME) operably linked to a promoter element, the chimeric promoter permaphent of interest, and (d) a vector comprising the chercologous molecule of interest, and (d) a vector comprising the sequence encoding a heterologous molecule of interest or increased continuous continuous continuous models and the nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or increased continuous continuous models and for constructing chimeric promoters for transgene sequence is useful for constructing chimeric promoters for transgene continuous and for driving high leavel expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heterologous molecule expression; plastid rRNA operon; Prrn promoter; transgenic plant; transgene expression; Prrn transcription modulating element; PTME; chimeric promoter; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of Prrn promoter derivative pJYS176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADT78224 standard; DNA; 112 BP.
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1 Similarity 87.5%;
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(SUZU/) SUZUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
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vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating prometer plants, comprising at least one Prrn transcription modulating prometer being further operably linked to a promoter element, the chimeric promoter. The nucleic acid sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type przn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 38.4; DB 13; Length 112; 87.5%; Pred. No. 0.00016; ive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 GTGGGATTGACGTGAGGGGGGGGGATGGCTATATTAGAGGGGGGGAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                               Sequence 112 BP; 33 A; 16 C; 42 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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  886666666666688888
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Heterologous molecule expression; plastid rRNA operon; Prrn promoter; transgenic plant; transgene expression; Prrn transcription modulating element; PTME; chimeric promoter; ds. DNA sequence of Prrn promoter derivative pJYS171. ADT78219 standard; DNA; 112 (first entry) 27-JAN-2005 ADT78219; ADT78219

15-DEC-2003; 2003US-00737251. 13-DEC-2002; 2002US-0433302P 04-NOV-2004.

JS2004221338-A1 Unidentified

(SUZU/) SUZUKI J Y. (MALI/) MALIGA P.

Suzuki JY; Maliga P,

WPI; 2004-774976/76.

The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid arRAA operon (Frrn) sequences given as SEO ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon qiven as SEO ID No: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (FTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression. Claim 1; SEQ ID NO 18; 34pp; English.

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chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prn promoter derivative.
                                                                                                                                                                                                                                                                                                                                                                           Heterologous molecule expression; plastid rRNA operon; Prrn promoter;
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; transgene expression;
Prrn transcription modulating element; PTME; chimeric promoter;
                                                                                                                                                          ö
                                                                                                                               61.0%; Score 38.4; DB 13; Length 112; llarity 87.5%; Pred. No. 0.00016; Conservative 0; Mismatches 6; Indels 0
                                                                                                                                                                                  63
                                                                                                                                                                                              GTGGGATTGACGTGAGGGGCTCCGATGGCTATATTTCTGGGAGCGAA 75
                                                                                                                                                                                 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATAGAGGGAGCGAA
                                                                                                      Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                   DNA sequence of Prrn promoter derivative pJYS119.
                                                                                                                                                                                                                                                                       ADT78211 standard; DNA; 112 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2003; 2003US-00737251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-2002; 2002US-0433302P
                                                                                                                                                                                                                                                                                                                         27-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maliga P, Suzuki JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-774976/76.
                                                                                                                         Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MALI/) MALIGA P.
(SUZU/) SUZUKI J Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004221338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2004.
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                                                                                                                                                                                                                                               RESULT 5
  88888888888888
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The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRM operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID Nos: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids to thigher plants, comprising at least one Prrn transgenes in plastids of element (PPME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a chimeric promoter. The nucleic acid sequence is operably linked to a sequence of the heterologous molecule of interest or its precursor. Sequence encoding a heterologous molecule is decreased or integers or its Expression of the heterologous molecule is decreased or integers or its precursor. The nucleic acid relative to that observed using wild-type Prrn sequence. The nucleic sequence is useful for constructing chimeric promoters for transgene

New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

Claim 1; SEQ ID NO 10; 34pp; English.

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The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID Nos: 31). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this cuctor, (c) a chimeric promoter for expression of transgenes in plastids celement (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a per enclogous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased a sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.
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expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heterologous molecule expression; plastid rRNA operon; Prrn promoter;
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; transgene expression;
Prrn transcription modulating element; PTME; chimeric promoter; ds.
                                                                                                                                                                             63
                                                                                                                                                                                                                25 GAGGTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA 75
                                                                                                                                       .;
0
                                                                                             58.1%; Score 36.6; DB 13; Length 112; 82.4%; Pred. No. 0.00074; ive 0; Mismatches 9; Indels 0
                                                                                                                                                                             13 GAGGTGGGATTGACGTGAGGGGCCTCCCTAGGCTATATAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;
                                                      Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence of Prrn promoter derivative pJYS118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 9; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002; 2002US-0433302P
                                                                                                                                                                                                                                                                                                                    ADT78210 standard; DNA; 112
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                           Query Match
Best Local Similarity 82.1.
Local 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-774976/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MALI/) MALIGA P.
(SUZU/) SUZUKI J Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004221338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce habbarmacuticals or fine chemicals, e.g. enzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a gene fragment shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                            Vegetable plastid transformation; transgenic; recognition sequence; plant; site-specific integration; nutrition; seed production; gene; chemical production; promoter; ds.
                                                          63
                                                                              TCCCTCGTGGGGATTGACGTGAGGGGGGGATGGCTATATTTCTGGGAGCGAA
                            o'
                                                          TCCGAGGTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
    Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GTGGGATTGACGTGAGGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 GTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAAA
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
    DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.6; DB 9;
Pred. No. 0.0096;
0; Mismatches 9
                  0.0035;
                              0; Mismatches
    Score 34.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 132; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUNG-) SUNGENE GMBH & CO KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                              ВР.
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2002; 2002WO-EP014303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2001; 2001DE-01063159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.3%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE34206 standard; DNA; 91
                                                                                                                                                              ACC85363 standard; DNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004 (first entry)
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                  N tabacum Prrn16 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.3
Best Local Similarity 81.2
Matches 39; Conservative
                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-541820/51.
    Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                WO2003054201-A1.
                                                                                                                                                                                                                    18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biesgen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE34206;
                                                            10
                                                                                                                                                                                         ACC85363;
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Heterologous molecule expression; plastid rRNA operon; Prrn promoter;

DNA sequence of Prrn promoter derivative pJYS181.

27-JAN-2005 (first entry)

transgenic plant; transgene expression; Prrn transcription modulating element; PTMB; chimeric promoter; ds.

15-DEC-2003; 2003US-00737251. 13-DEC-2002; 2002US-0433302P.

US2004221338-A1. 04-NOV-2004. Waliga P, Suzuki JY; WPI; 2004-774976/76.

(MALI/) MALIGA P. (SUZU/) SUZUKI J Y.

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This invention describes a novel method for integrating a DNA sequence into the plastid DNA of a multicellular plant or its derived cells and for selecting homortansplastoric cells or plants. The method comprises inducing DNA double-strand breaks in plant plastid DNA, which contains at least one recognition site for targeted induction of such breaks, by treating the plant or its cells with an enzyme able to create these breaks and a transformation construct that contains an insertion sequence breaks and a transformation construct that contains an insertion sequence. The plastid DNA so that the function of the creognition site for targeted induction of breaks is inserted into the plastid DNA so that the function of the creognition sequence has been inserted are then selected. Transgenic plants in which the DNA sequence has been inserted are then selected. Transgenic plants or insertion sequence has been inserted are then selected. Transgenic plants in which the DNA sequence has been inserted are then selected. Transgenic plants or transmis, amino acids, flavourings and aromatising agents, dyes, antibodies and vaccines. The method eliminates the need for antibodies and vaccines. The method eliminates the need for antibodies and vaccines. The method eliminates the need for conting homotransplastomic plants. The genetic constructs used are producing homotransplastomic plants. The genetic constructs used are construct saine and since plastid DNA. Foreign DNA will not be transferred in pollen control of a since plastid but aromatezed in pollen control of a since plastid seemble control of a since plastid seemble control of a since plastid seements on the control of a since plastid seements on the sone of proderives.
                                         plastid; plant; homotransplastomic cell; insertion sequence; nutrition; seed production; enzyme; vitamin; amino acid; flavouring; aromatising agent; dye; antibody; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for integrating DNA into plant plastids, useful for making transgenic plants for e.g. food or animal feed, by inducing targeted double-strand DNA breaks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%; Score 33.6; DB 10; Length 91; 81.2%; Pred. No. 0.0096; ive 0; Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 46; 182pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    under control of a single promoter.
                                                                                                                                                                                                                                                                                                                                                                   (SUNG-) SUNGENE GMBH & CO KGAA
                                                                                                                                                                                                                                                                                                                        20-DEC-2001; 2001DE-01063161.
                                                                                                                                                                                                                                                                       16-DEC-2002; 2002WO-EP014302.
  Tobacco Prrn16 promoter DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-541816/51.
                                                                                                                                  Nicotiana tabacum,
                                                                                                                                                                              WO2003054189-A2.
                                                                                                                                                                                                                              03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                 Biesgen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

Claim 1; SEQ ID NO 28; 34pp; English.

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The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences of given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (Given as SEQ ID Nos: 51). Also disclosed are (a) a wector comprising the nucleic acid sequence above, (b) a transpenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating clement (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a computer. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Comprising the heterologous molecule is decreased or increased crelative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene computers of prints and for driving high level expression of heterologous proteins of the expression and for driving high level expression of heterologous proteins of the expression of preserved using wild-type Prrn expression and for driving high level expression of heterologous proteins of the expression and for driving high level expression of heterologous proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATTAGAGGGAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence of Prrn promoter derivative pJYS183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.01;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 81.2%;
Conservative
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Best Local Similarity
Matches 39; Conserv
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Gaps

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81

GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63

39; Conservative

Matches

16

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Similarity

GTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA

ADT78229 standard; DNA; 112 BP.

RESULT 9 ADT78229 ADT78229:

US2004221338-A1.

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The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID Nos: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising the nucleic acid sequence above, (c) a transgenic plant comprising the corp. (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transscription modulating or lement (PPME) operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or interested 
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Prrn transcription modulating element; PTME; chimeric promoter; ds.
molecule expression; plastid rRNA operon; Prrn promoter;
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                           transgenic plant, transgene expression;
Prrn transcription modulating element; PTME; chimeric promoter; ds.
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Les 39; Conservative
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(SUZU/) SUZUKI J Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences
                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
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Prn transcription modulating element, PTME; chimeric promoter; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of Prrn promoter derivative pJYS182.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 27; 34pp; English
                                                                                                    15-DEC-2003; 2003US-00737251.
                                                                                                                                              13-DEC-2002; 2002US-0433302P
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                 WPI; 2004-774976/76.
                                                                                                                                                                                      (MALI/) MALIGA P.
(SUZU/) SUZUKI J Y.
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The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences of given as SEQ ID Nos: 4-30 in the specification, or which may comprise given as SEQ ID Nos: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising the nucleic acid sequence above, (b) a transgenic plant comprising this comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a component being further operably linked to a sequence encoding a chimeric promoter. The nucleic acid sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased confinence contains a heterologous molecule is decreased or increased contains a part observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene contains a part promoter derivative.
                                                                                                                                                              New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
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Prrn transcription modulating element; PTME; chimeric promoter; ds.
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81.2%; Pred. No. 0.01;
live 0; Mismatches
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                                                              Suzuki JY;
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                                                                                                                 WPI; 2004-774976/76.
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        (SUZU/) SUZUKI J Y.
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(SUZU/) SUZUKI J Y.
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                                                              Maliga P,
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Matches
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Prrn transcription modulating element; PTME; chimeric promoter; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 29; 34pp; English.
15-DEC-2003; 2003US-00737251.
                                                  13-DEC-2002; 2002US-0433302P.
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                                                                                                   (MALI/) MALIGA P.
(SUZU/) SUZUKI J Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2004221338-A1
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Matches

RESULT 13

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Gaps

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9; Indels

63

DB 13; Length 112;

The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise (given as SEQ ID Nos: 51). Also disclosed are (a) a vector omprising the nucleic acid sequence above, (b) a transgenic plant comprising the nucleic acid sequence above, (c) a transgenic plant comprising the sector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transscription modulating colement (PTME) operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or interested or i relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins n plastids. The present sequence represents a Prrn promoter derivative. New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression. Sequence 112 BP; 31 A; 17 C; 41 G; 23 T; 0 U; 0 Other; Disclosure; SEQ ID NO 3; 34pp; English.

; 0 / Match 53.3%; Score 33.6; DB 13; Length 112; Local Similarity 81.2%; Pred. No. 0.01; es 39; Conservative 0; Mismatches 9; Indels 0; 63 GTGGGATTGACGTGAGGGGCCTCCCTAGGCTATATTAGAGGGAGCGAA 16 Query Match Matches ò

28 GTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA 75

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Gaps

ADT78208 standard; DNA; 112 (first entry) 27-JAN-2005 ADT78208; RESULT 15 ADT78208

BP.

DNA sequence of Prrn promoter derivative pJYS116.

Heterologous molecule expression; plastid rRNA operon; Prrn promoter; transgenic plant; transgene expression; Prrn transcription modulating element; PTME; chimeric promoter;

Unidentified

US2004221338-A1.

04-NOV-2004.

13-DEC-2002; 2002US-0433302P.

15-DEC-2003; 2003US-00737251.

(MALI/) MALIGA P. (SUZU/) SUZUKI J Y.

Suzuki JY; daliga P,

WPI; 2004-774976/76.

New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

Limited Formation Comparison of the Comparison of the Chimeric promoter being further operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type prns sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prnn promoter derivative. The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEO ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEO ID No: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising the vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modilating ö Query Match 53.3%; Score 33.6; DB 13; Length 112; Best Local Similarity 81.2%; Pred. No. 0.01; Matches 39; Conservative 0; Mismatches 9; Indels 0; 63 28 graddatrakadadadadadanadaratrircraddadada 75 16 GTGGGATTGACGTGAGGGGCTCCCTAGGCTATATTAGAGGGAGCGAA Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other; Claim 1; SEQ ID NO 7; 34pp; English $\overset{\times}{\times}$ ò

Search completed: February 21, 2006, 05:38:11 Job time : 283 secs

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Gaps

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AX798146 Sequence
CX114516 Sequence
CX114516 Sequence
CX010451 Sequence
EX1179 Process for
AX137514 Sequence
AX137514 Sequence
AX137514 Sequence
AX137514 Sequence
AX137514 Sequence
AX137514 Sequence
AX77661 Sequence
AX77662 Sequence
AX242682 Sequence
AX242682 Sequence
AX319835 Sequence
AX19835 Sequence
                                                         February 21, 2006, 05:35:59; Search time 2168 Seconds (without alignments) 1651.816 Million cell updates/sec
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                                                                                                                        1 gagctcttctccgaggtggg......gctatattagagggagcgaa 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                  11766282
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                          5883141 seqs, 28421725653 residues
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      OM nucleic - nucleic search, using sw model
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CS114516
CS001461
ES1179
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BD174932
AX07661
CQ797808
AR145914
AR242682
AR568182
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                                                                                                                                            IDENTITY NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                   US-10-737-251-51
63
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Match Length DB
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9b_in:*
9b_om:*
9b_om:*
9b_pb.:*
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9b_ro:*
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9b_mr:*
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1112...
154...
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Perfect score:
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                                                            Run on:
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No.
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| AX537601 Sequence BD247598 Methods f AR58183 AR58183 Sequence AX319836 AR31983 Sequence AX319836 AR31983 Sequence AR171710 AR31983 Sequence CQB28073 CQB28073 Sequence CQB28073 CQB28073 Sequence CQB28073 CQB28073 Sequence CQB3028 AX798312 Sequence AX798312 AX798312 Sequence AX38829 AX798312 Sequence CQB30289 Sequence CQB30289 CQB30289 Sequence CQB30289 CQB30289 Sequence CQB30280 CQB303141 Sequence CQB28069 CQB30280 Sequence CQB28069 CQB28069 Sequence CQB28069 CQB28069 Sequence CQB28069 CQB28069 Sequence CQB28069 CQB28070 Sequence CQB30287 CQB28070 Sequence CQB30287 Sequence AX798126 Sequence AX798126 Sequence | AR36883 CC083029 CQ83029 CQ82807 CQ82807 VQ0165 6 AJZ786 ENTS | 91 bp DNA linear PAT 08-OCT-2003 w003054201. on tobacco) e; Streptophyta; Embryophyta; Tracheophyta; phyta; eudicotyledons; core eudicotyledons; nales; Solanaceae; Nicotiana. mation of vegetable plastids 2 03-JUL-2003; (DB) fiers otiana tabacum" | /db_xrer="taxon:4097" 191 | 91 bp DNA linear PAT 08-OCT-2003 |
|---|--|---|--|--|
| 220 6 W 224 6 W 2244 | 6 6 6 115 115 | 91 b) 2.2 from Patent W00305; 3.1 GI:37604427 1a tabacum (common tobaca tabacum, as 'viridiplantae; Strepphyta; Magnoliophyta; ophyta; Magnoliophyta; lamiids; Solanales; % lamiids; Solanales; % c. C. C. KgAA (DE) Location/Qualifiers 1. 91 Corganism="Nicotiana tabula & Co. KgAA (DE) Location/Qualifiers 1. 91 Corganism="Nicotiana tabula & Co. KgAA (DE) Location/Qualifiers Corganism="Nicotiana tabula & Co. KgAA (DE) Location/Qualifiers Corganism="Nicotiana tabula & Co. KgAA (DE) Co. KgAA | 9 0 2 | 6 from Patent GI:37605006 |
| | | AX798146 Sequence 22 from P AX798146.1 GI:376 Nicotiana tabacum Nicotiana tabacum Nicotiana tabacum Sukaryota, Viridip Spermatophyra; Maga asterids; lamiids; Biesgen,C. Method for the tra Parent: WO 0305420 Sungene GmbH & Co. Location/ 1. 91 /organism /mol type | er ch 1 S 39 | AX798954 Sequence 46 AX798954 AX798954.1 |
| 000000000000000000000000000000000000000 | | RESULT 1 AX798146 LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE | promoter ORIGIN Query Match Best Local Matches 3 Qy 16 | RESULT 2 AX798954 LOCUS DEFINITION ACCESSION VERSION |

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Gaps

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Nicotiana tabacum (common tobacco)

Nicotiana tabacum

Nicotiana tabacum

Nicotiana tabacum

Nicotiana tabacum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

E 1 (bases 1 to 127)

Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.

Method for transforming plant and transformed plant

L Patent: JP 2001046073-A 16 20-FEB-2001;

RIKAGAKU KENKYUSHO, HIDEO NAKASHITA

OS Nicotiana tabacum (tobacco)

PN JP 2001046073-A/16

PD 20-FEB-2001

PP 09-AUG-1999 JP 1999225832
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 GTGGGATTGACGTGAGGGGCAGGATGGTTATTTCTGGGAGCGAA 88
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     Cox, K.M. and Peele, C.G.
Chloroplast transformation of duckweed
Patent: WO 2005005643-A 20-JAN-2005;
Biolex, Inc. (US)
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                                                                                                                                                                                   /organism="Nicotiana tabac
/mol_type="unassigned DNA"
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Process for producing polyester.
ES1197
ES1197.1 GI:18629514
JP 2001046074-A/16.
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JP 2001046073-A/16.
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Best Local Similarity
Matches 39; Conserv
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VERSION
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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81.2%; Pred. No. 0.097;
ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 91;
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Methods for the transformation of vegetal plastids
Patent: WO 03054189-A 46 03-JUL-2003;
Sungene GmbH & Co. KgAA (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GTGGGATTGACGTGAGGGGCCTCCTAGGCTATATTAGAGGGAGCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="plastidic promoter Prrn16"
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1. 113
Arguments sea synthetic construct "
| mol type = unassigned DNA" |
| db_xref="taxon:32630" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Controlling gene expression in plastids Patent: WO 2005054481-A 13 16-JUN-2005; Icon Genetics AG (DE)
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                                                                                                                                                                                                                                                                                                                     1. .91
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/db zref="taxon:4097"
1. .91
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Sequence 13 from Patent WO2005054481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6 from Patent WO2005005643.
CS001461
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                               Nicotiana tabacum (common tobacco)
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                                                           Nicotiana tabacum
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Best Local Similarity
Matches 39; Conserva
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CS114516
  KEYWORDS
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Gaps

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63

PAT 31-JAN-2002

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; saterids; lamidas; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 142)

2 Tomizawa, K. and Yokota, A.

A system for expressing protein using plants

A system for expressing protein using plants

A system arbacum (tobacco)

Nicotiana tabacum (tobacco)

PN JP 2002272476-A/2

PP 22-MAR-2001

PP 22-MAR-2001

PP 22-MAR-2001

PP 22-MAR-2001

PP CI2NIS/00,CO7K14/415,CI2N5/10,CI2NIS/00,CI2NS/00 CC
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                                                                      Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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/organism='Nicotiana tabacum (tobacco)'.
Location/Qualifiers
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                                                                                                                                                                         Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
Methods for transformation of plants, transformed plants and
processes for preparation of polyesters
Patent: EP 1076095-A 16 14-FEB-2001;
Riken (JP)
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A system for expressing protein using plants.
BD174932
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Pred. No. 0.097;
0; Mismatches
                                                                                                                                                                                                                                                                                 1. .127
/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"

    1. .142
    /organism="Nicotiana tabacum"

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JP 2002272476-A/2.
Nicotiana tabacum (common tobacco)
       Sequence 16 from Patent EP1076095
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/db_xref="taxon:4097"
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                                     AX137514.1 GI:14273708
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ilarity 81.2%;
Conservative 0
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Best Local Similarity
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                                     Embryophyta; Tracheophyta;
edons; core eudicotyledons;
                                                                                                                                          RIKAGAKU KENKTUSHO
OS Nicotiana tabacum (tobacco)
OS 1201046074-A/16
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225839
PR HIDBO NAKASHITA,ISAMU YAMAGUCHI,KEIKO YOSHIOKA,YOSHIHARU DOI
PC C12N15/09,A01H5/09,C12N5/10,C12N9/10,C12N9/10,C12N9/62,PC
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Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
Methods for transformation of plants, transformed plants and
processes for preparation of polyesters
Patent: US 6620601-A 16 16-SEP-2003;
Riken; Saitama;

    127 /organism='Nicotiana tabacum (tobacco)'

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Nicotiana tabacum (common tobacco)

Nicotiana tabacum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu asterids; lamiids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 127)
Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
Process for producing polyester
Patent: JP 2001046074-A 16 20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
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81.2%; Pred. No. 0.097;
iive 0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 from patent US 6620601.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:4097"
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 81.2
Matches 39; Conservative
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AR399398
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/organism="unknown"
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Best Local Similarity
Matches 39; Conserv
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//organisma="synthetic construct"
//mol type="unassigned DNA"
//db_xref="taxon:32630"
//db_xref="taxon:32630"
//note="bescription of Artificial Sequence: Synthetic DNA fragment codifying for the promoter region of the plastid 16S ribosomal RNA (Prrn), with added restriction sites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selman-housein Sosa,G., aguiar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz Lez,O. Vector for the production of transplastomic angiosperm plants Patent: WO 2004029256-A 14 08-APR-2004; CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU) Location/Qualifiers
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Enhanced expression of proteins using gfp
Patent: WO 0104331-A 1 18-JAN-2001;
Calgene LLC (US)
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Pred. No. 0.096;
0; Mismatches
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Pred. No. 0.097;
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other sequences; artificial sequences.
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CQ797808

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AR145914
AR145914.1 GI:15109103
                                    AX076661 168 bp Sequence 1 from Patent WO0104331.
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AX076661.1 GI:12711193
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Unknown.
Unclassified.
1 (bases 1 to 201)
Maliga,P., Allison,L.A. and Hajdukiewicz,P.T.
Nuclear-encoded transcription system in plastids of higher plants
Parent: US 6472586-A 58 29-0CT-2002;
Parent: US 6472586-A 58 29-0CT-2002;
Phtgers, The State University of New Jersey; Piscataway, NJ
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 184)
Bogosian, G., O'Neil,J.P. and Staub,J.M.
Bacterial expression systems based on plastic or mitochondrial promoter combinations
promoter 10 6218145-A 3 17-APR-2001;
Location/Qualifiers
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Best Local Similarity 81.2%; Pred. No. 0.096;
Matches 39; Conservative 0; Mismatches 9; Indels 0
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Unclassified.
Unclassified.
1 (bases 1 to 202)
Staub,J.M., Ye,G. and Broyles,D.L.
Method for the transformation of plant cell plastids
Patent: US 6781033-A 1 24-AUG-2004;
Monsanto Technology LLC; St. Louis, MO;
                                                                                                                                                                                                                                                                                                                                                                                                                     42 GTGGGATTGACGTGAGGGGCAGGGATGGCTATATTTCTGGGAGCGAA
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Sequence 58 from patent US 6472586.
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Sequence 1 from patent US 6781033.
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                                                                                                                Query Match 53.3%; Score 33.6; DB 6; Length 202; Best Local Similarity 81.2%; Pred. No. 0.096; Matches 39; Conservative 0; Mismatches 9; Indels
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Enhanced expression of proteins using gfp
Patent: WO 0104331-A 2 18-JAN-2001;
Calgene LLC (US)
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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AX076662 AX076662.1 GI:12711194
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